CLAIMS

We claim:

1. A method of mapping surface epitopes on a target protein comprising:

a) providing a solid support comprising an antibody capable of binding to said target protein;

b) contacting said solid support with a library of random peptides under conditions where a set of probe peptides bind to said antibody;

c) eluting said set of probe peptides;

determining the amino acid sequence of the members of said set of probe peptides;

e) computationally aligning said probe peptide sequences to said target protein;

f) generating a set of best alignments for each probe peptide sequence;

g) generating a surface-neighbor probability graph from said alignments;

h) determining edge weight of said surface-neighbor probability graph;

i) constructing a at least one surface epitope of said target protein from said surface-neighbor probability graph.

2. The method according to claim 1, wherein said surface epitope comprises a discontinuous epitope.

3. The method according to claim 1, wherein said computational aligning comprises a branch and bound program.

4. The method according to claim 1, wherein said library comprises a phage display library.

5. The method according to claim 4, wherein said method further comprises enriching said phage display library.

6. The method according to claim 1, wherein said method further comprises amplifying said set of probe peptides prior to said determining of amino acid sequence.

7. A method of mapping discontinuous epitopes on a target protein comprising:

a) providing a solid support comprising an antibody capable of binding to said target protein;

b) contacting said solid support with a library of random peptides under conditions where a set of probe peptides bind to said antibody;

c) eluting said set of probe peptides;

d) determining the amino acid sequence of the members of said set of probe peptides;

e) computationally aligning the amino acid sequences of said probe peptide sequences to said target protein;

f) constructing at least one discontinuous epitope on said target protein.

8. The method according to claim 7, wherein said computational aligning comprises a branch and bound program.

9. The method according to claim 7, wherein said library comprises a phage display library.

10. The method according to claim 9, wherein said method further comprises enriching said phage display library.

11. The method according to claim 7, wherein said method further comprises amplifying said set of probe peptides prior to said determining of amino acid sequence.

12. A method of mapping discontinuous epitopes on a target protein comprising:

a) providing a solid support comprising an antibody capable of binding to said target sequence;

b) contacting said solid support with a library of random peptides under conditions where a set of probe peptides bind to said antibody;

c) eluting said set of probe peptides;

d) determining the amino acid sequence of the members of said set of probe peptides;

e) determining a consensus epitope sequence;

f) computationally aligning said consensus epitope sequence to said target protein;

g) constructing at least one discontinuous epitope on said protein.

13. The method according to claim 12, wherein said computational aligning comprises a branch and bound program.

14. The method according to claim 12, wherein said library comprises a phage display library.

15. The method according to claim 14, wherein said method further comprises enriching said phage display library.

16. The method according to claim 12, wherein said method further comprises amplifying said set of probe peptides prior to said determining of amino acid sequence.

17. A method of mapping surface epitopes on a target protein comprising:

a) providing a solid support comprising an aptamer capable of binding to said target protein;

b) contacting said solid support with a library of random peptides under conditions where a set of probe peptides bind to said antibody;

c) eluting said set of probe peptides;

determining the amino acid sequence of the members of said set of probe peptides;

e) computationally aligning said probe peptide sequences to said target protein;

f) generating a set of best alignments for each probe peptide sequence;

g) generating a surface-neighbor probability graph from said alignments;

h) determining edge weight of said surface-neighbor probability graph;

i) constructing at least one surface epitope of said target protein from said surface-neighbor probability graph.

18. A method of mapping discontinuous epitopes on a target protein comprising:

a) providing a solid support comprising an aptamer capable of binding to said target sequence;

b) contacting said solid support with a library of random peptides under conditions where a set of probe peptides bind to said antibody;

c) eluting said set of probe peptides;

d) determining the amino acid sequence of the members of said set of probe peptides;

e) determining a consensus epitope sequence;

f) computationally aligning said consensus epitope sequence to said target protein;

g) constructing at least one discontinuous epitope on said protein.

19. A method of mapping protein-protein binding sites comprising:

a) providing a solid support comprising a first protein;

contacting said solid support with a second protein under conditions where said first protein binds to said second protein;

c) contacting said solid support with a library of random peptides under conditions where a set of probe peptides compete with said second protein for binding to said first protein;

d) eluting said set of probe peptides;

e) determining the amino acid sequences of the members of said set of probe peptides;

f) computationally aligning said amino acid sequences of the members of said set of probe peptides to said target protein;

g) constructing the binding site on said protein.